

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:09:14 ; Search time 8498.8 Seconds
(without alignments)
36.667 Million cell updates/sec

Title: US-09-851-670-5

Perfect score: 29

Sequence: 1 ttgcttggtgctgctgctgtttca 29

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:

11351937 seqs, 537289281 residues

Total number of hits satisfying chosen parameters:

111874

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estlin:*
4: em_estlom:*
5: em_estlpl:*
6: em_estba:*
7: em_estro:*
8: em_estrov:*
9: em_hlc:*
10: gb_estcl:*
11: gb_estl2:*
12: gb_hlc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.4	60.0	50	10	AU105368 AU105368
2	15.8	54.5	35	13	BH023779 BC02293-3
3	15.4	53.1	54	13	AZ447232 IM0244L13
4	15.2	52.4	40	13	CNS06VE6 AL1417028 T3 end of
5	15.2	52.4	44	13	AZ505846 AL0346P07
6	15.2	52.4	55	10	AA906735 OK78H04.S
7	15.2	52.4	56	13	AZ930011 479.d1157
8	15.1	51.7	26	13	AZ307056 IM0008G23
9	14.8	51.0	36	13	AZ330732 IM0056F12
10	14.8	51.0	39	13	AZ330739 IM0056F12
11	14.8	51.0	58	13	AZ424808 IM0204A07
12	14.8	51.0	60	10	AA405801 z457f07.s

13	14.6	50.3	40	13	AZ391073	AZ391073 IM0152124
14	14.6	50.3	58	13	AZ661852	AZ661852 IM0540F07
15	14.4	49.7	41	13	AZ459776	AZ459776 IM0264A19
16	14.4	49.7	52	10	AA894517	AA894517 cF90805.S
17	14.2	49.0	29	13	AZ827060	AZ827060 IM0103F17
18	14.2	49.0	32	13	AZ627466	AZ627466 IM0469I13
19	14.2	49.0	34	13	AZ626219	AZ626219 IM0466B23
20	14.2	49.0	36	10	AM248008	AM248008 2820129..3
21	14.2	49.0	37	13	AZ820288	AZ820288 2M0092G19
22	14.2	49.0	38	13	AZ819005	AZ819005 2M0089F23
23	14.2	49.0	40	10	AA888211	AA888211 cF86d11.S
24	14.2	49.0	41	13	AZ356235	AZ356235 IM0097D16
25	14.2	49.0	43	10	A1018532	A1018532 cu24g12.x
26	14.2	49.0	45	13	AZ634992	AZ634992 IM0451A08
27	14.2	49.0	46	11	T25667	T25667 EST00536.B4
28	14.2	49.0	50	10	AU103997	AU103997 AU103997
29	14.2	49.0	50	10	BE732496	BE732496 601567696
30	14.2	49.0	50	11	BG538913	BG538913 602568565
31	14.2	49.0	51	11	C00246	C00246 HUMCS000591
32	14.2	49.0	52	10	AM410447	AM410447 FH06C03.Y
33	14.2	49.0	55	11	BG694530	BG694530 NISC_1v03
34	14.2	49.0	60	10	AW058965	AW058965 fe14d12.x
35	14.2	48.3	38	11	H99519	H99519 yx29b12.s1
36	14.2	48.3	43	13	AZ960584	AZ960584 2M0228M07
37	14.2	48.3	50	13	AQ025638	AQ025638 1(2)05488
38	13.8	47.6	52	10	AA626479	AA626479 ab50a01.r
39	13.8	47.6	55	13	AZ333386	AZ333386 IM0062N23
40	13.8	47.6	55	13	AZ658522	AZ658522 IM0535A18
41	13.8	47.6	58	13	AZ537183	AZ537183 AST-2P026
42	13.6	46.9	36	13	AZ853353	AZ853353 2M0156D06
43	13.6	46.9	43	10	A1540308	A1540308 tg34e02.x
44	13.6	46.9	44	13	AQ074129	AQ074129 ER(X)1612
45	13.6	46.9	49	13	AZ876952	AZ876952 2M0192E12

ALIGNMENTS

RESULT 1	AU105368	50 bp	mRNA	EST	05-Apr-2001
LOCUS	AU105368	Sugano Homo sapiens	CDNA library	Homo sapiens	CDNA clone
DEFINITION	HEMB0039	mRNA sequence.			
ACCESSION	AU105368				
VERSION	AU105368.1	GI:13554889			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.				
TITLE	Fine structural analysis of transcription start sites of human				
JOURNAL	mRNAs using full-length enriched and 5'-end enriched cDNA libraries				
COMMENT	Unpublished (2001)				
CONTACT	Yutaka Suzuki				
DEPARTMENT	Department of Medical Science, University of Tokyo				
INSTITUTE	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan				
EMAIL	ysuzuki@ems.u-tokyo.ac.jp				
FEATUERS	Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S.				
SOURCE	Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).				
LOCATION	Location/Qualifiers				
1..50	/organism="Homo sapiens"				
/db_xref="taxon:9606"					
/clone="HEMB0039"					
/clone_id="Sugano Homo sapiens					
CDNA library"					
BASE COUNT	9 a	7 c	11 g	22 t	1 others
ORIGIN					

Query Match	60.0%	Score 17.4	DB 10	Length 50
Best Local Similarity	75.0%	Pred. No. 2.2e+04		
Matches 21: Conservative	0	Mismatches 7	Indels 0	Gaps 0

Oy	2	ttggcttgatcgtctgcgtctgttca 29		
Db	15	TTGCNTATGGCCATTGTTTGTTTTAA 42		

RESULT	2			
BH023779				
LOCUS				
DEFINITION		BH023779 35 bp DNA GSS 09-JUL-2001		
ACCESSION		BC022933-3orfme Drosophila melanogaster P[GT1] P element insertion		
VERSION		lines Drosophila melanogaster genomic Sequence recovered from 3'		
KEYWORDS		end of P element, DNA sequence.		
SOURCE		BH023779.1 GI:14627238		
ORGANISM		GSS.		
		fruit fly.		
REFERENCE		Drosophila melanogaster		
AUTHORS		Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
		Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;		
		Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
		1 (bases 1 to 35)		
		Levis,R., Hoskins,R., Liao,G., Mozer,N., Tsang,G., He,Y., Karpen		
		G., Bellen,H., Rubin,G., and Spradling,A.		
		The Berkeley Drosophila Genome Project Gene Disruption Project		
TITLE		Unpublished (2001)		
JOURNAL		Contact: Gerald Rubin		
COMMENT		Berkeley Drosophila Genome Project		
		University of California, Berkeley		
		LSA Building, Berkeley, CA 94720-3200, USA		
		Fax: 5106433947		
		Email: gerry@fruitfly.berkeley.edu		
		Sequence recovery method was inverse PCR.		
		Sequence orientation is forward strand relative to 5' end of P		
		element		
		The P element insertion position is base 1 in the 35 bases. This		
		insertion position refers to the first base of the 8 base target		
		recognition sequence.		
		Class: transposon-tagged.		
FEATURES		location/Qualifiers		
source		1..35		
		/organism="Drosophila melanogaster"		
		/db_xref="taxon:7227"		
		/clone_lib="Drosophila melanogaster P[GT1] P element		
		insertion lines"		
		/note="Inverse PCR was performed on Drosophila		
		melanogaster strains each of which contains one or more		
		P[GT1] P-element transposon insertion. The resultant		
		fragment for each strain was directly sequenced to		
		determine the genomic sequence at the site of insertion.		
		Details of the protocols used can be found at		
		http://www.fruitfly.org/about/methods/inverse.pcr.html."		
BASE COUNT		0 a 12 c 9 g 14 t		
ORIGIN				

Query Match	54.5%	Score 15.8	DB 13	Length 35
Best Local Similarity	74.1%	Pred. No. 7.9e+04		
Matches 20: Conservative	0	Mismatches 7	Indels 0	Gaps 0

Oy	2	ttggcttgatcgtctgcgtctgttc 28		
Db	7	TTGCGTTCGTCGCTGCTTGCTTTGC 33		

RESULT	3			
LOCUS		AZ447232 54 bp DNA GSS 04-OCT-2000		
DEFINITION		IM0244113f Mouse 10kb plasmid UUGC1M library Mus musculus genomic		

ACCESSION	Clone UUGC1M0244L13 F, DNA sequence.	
VERSION	A2447232	
KEYWORDS	A2447232.1 GI:10599012	
SOURCE	GSS.	
ORGANISM	house mouse.	
REFERENCE	Mus musculus	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE	1 (bases 1 to 54)	
JOURNAL	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.	
COMMENT	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
	Unpublished (2000)	
	Contact: Robert B. Weiss	
	University of Utah Genome Center	
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA	
	Tel: 801 585 5606	
	Fax: 801 585 7177	
	Email: ddunn@genetics.utah.edu	
	Insert Length: 10000 Std Error: 0.00	
	Plate: 0244 row: L column: 13	
	Seq primer: CGTCTAAACGACGCGCCAGT	
	Class: Plasmid ends	
	High quality sequence stop: 54.	
FEATURES	Location/Qualifiers	
source	1..54	
	/organism="Mus musculus"	
	/strain="C57BL/6J"	
	/db_xref="taxon:10090"	
	/clone="UUGC1M0244L13"	
	/clone_lib="Mouse 10kb plasmid library"	
	/sex="Male"	
	/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"	
	/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource	
	(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114[gblAF29072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
BASE COUNT	28 a 11 c 4 g 11 t	
ORIGIN	11 c 11 t	
Query Match	53.1%; Score 15.4; DB 13; Length 54;	
Best Local Similarity	76.0%; Pred. No. 1e+05;	
Matches 19; Conservative	0; Mismatches 6; Indels 0; Gaps 0;	
0y	5 gcttgatcgctgcgttcgttca 29	
Db	33 gcttgatcgctgcgttcgttca 9	
RESULT 4	CNS06VE6 40 bp DNA GSS 06-JUL-2001	
CNS06VE6	GSS	
LOCUS	GSS	

DEFINITION T3 end of clone AX0A019F02 of library AX0A from strain CBS 7064
 of *Pichia farinosa*, genomic survey sequence.
 ACCESSION AL417028
 VERSION AL417028.1 GI:12198231
 LOCUS GSS.
 KEYWORDS *Pichia farinosa*.
 SOURCE *Pichia farinosa*
 ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; *Pichia*.
 REFERENCE 1 (bases 1 to 40)
 AUTHORS de Montigny, J., Spohner, C., Souciet, J., Tekala, F., Dujon, B., Wincker, P., Artiguenave, F., and Potier, S.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 15. *Pichia sorbitophila*
 JOURNAL FEBS Lett. 487 (1), 87-90 (2000)
 MEDLINE 20584725
 REFERENCE 2 (bases 1 to 40)
 AUTHORS Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G., Bojotin-Fukuhara, M., Bon, E., Brothier, P., Casaregola, S., de Montigny, J., Dujon, B., Durrens, P., Leplinge, A., Lorente, B., Malpertuy, A., Neuvéglise, C., Ozler-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffiano-Nioche, C., Wesolowski-Louvel, M., Wincker, P., and Weissenbach, J.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
 JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
 MEDLINE 20584711
 REFERENCE 3 (bases 1 to 40)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequef@genoscope.cns.fr - Web: www.genoscope.cns.fr)
 COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *varium*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
 FEATURES
 Source Location/Qualifiers
 1..40
 /organism="Pichia farinosa"
 /strain="CBS 7064"
 /db_xref="taxon:4920"
 /clone="AX0A019F02"
 /clone_lib="AX0A"
 /note="end: '73'"
 BASE COUNT 0 a 9 c 4 g 26 t 1 others
 ORIGIN
 Query Match 52.4%; Score 15.2; DB 13; Length 40;
 Best Local Similarity 71.4%; Pred. No. 1.2e+05;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 1 ttggcttgctgctgctgctgcttctc 28
 ||||| ||| | | | ||||| |||||
 Db 3 TTGGCTTCGTTTTCCTCTTTTTC 30
 RESULT 5
 A2505846 44 bp DNA GSS 05-OCT-2000
 LOCUS IM0346P07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0346P07 R, DNA sequence.
 ACCESSION A2505846
 VERSION A2505846.1 GI:10687162
 KEYWORDS GSS.
 SOURCE house mouse.

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 44)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weis, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0346 row: P column: 07
 Seq primer: CACACAGCAACGCTATGACC
 Class: Plasmid ends
 High quality sequence stop: 44.
 FEATURES
 Source Location/Qualifiers
 1..44
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0346P07"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, p1-resistant, F-"
 /note="Vector: pMD42ny; Purified genomic DNA from M. musculus (C57BL/6J male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321149b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT 15 a 12 c 8 g 9 t
 ORIGIN
 Query Match 52.4%; Score 15.2; DB 13; Length 44;
 Best Local Similarity 71.4%; Pred. No. 1.2e+05;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 2 ttggcttgctgctgctgcttcttca 29
 | ||||| || | ||||| || ||
 Db 39 TGGGCTTTGGACGCTTATCTTTTCACA 12
 RESULT 6
 AA906735 55 bp mRNA EST 24-AUG-1998
 LOCUS OK78H04.s1 NCI-CGAP-CC4 Homo sapiens cDNA IMAGE:1520119 3'
 DEFINITION similar to TR:Q34192 Q34192 NAH DEHYDROGENASE SUBUNIT 5. ; mRNA sequence.
 ACCESSION AA906735
 VERSION AA906735.1 GI:3042321

KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eumaxipota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
AUTHORS	Contact: Robert Strausberg, Ph.D. Email: ccgaps-r@mail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.
TITLE	CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLB at: www-bio.lnl.gov/bdbp/image/Image.html
JOURNAL	
COMMENT	
FEATURES	Trace considered overall poor quality Insert Length: 378 Std Error: 0.00 Seq primer: -40ml3 fwd. RT from Amersham High quality sequence stop: 1. Location/Qualifiers 1..55 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1520119" /clone_lib="NCI-CGAP_GCA" /russue_type="pooled germ cell tumors" /lab_host="DH10B" /note="Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(CT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT	0 a 4 c 11 g 40 t
ORIGIN	
Query Match	52.4%; Score 15.2; DB 10; Length 55;
Best Local Similarity	71.4%; Pred. No. 1.2e+05;
Matches	20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY	1 tttagcttgatcggtcgtctgttttc 28 Db 26 TTTTGCTTTGTCTTTCGTCTTTTTC 53
RESULT	7
LOCUS	A2930011 56 bp DNA GSS 01-APR-2001
DEFINITION	479.dl15f11.s1 Saccharomyces kluyveri Saccharomyces kluyveri
ACCESSION	A2930011 genomic clone 479.dl15f11.sl. DNA sequence.
VERSION	A2930011.1 GI:13500919
KEYWORDS	GSS.
SOURCE	Saccharomyces kluyveri.
ORGANISM	Saccharomyces kluyveri Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. 1 (bases 1 to 56) Clifton,P.F., Hillier,L.W., Fulton,L., Graves,T., Miner,T., Gish W.R., Waterston,R.H. and Johnston,M. Surveying Saccharomyces genomes to identify functional elements by comparative DNA sequence analysis Unpublished (2001) Contact: Johnstone M
JOURNAL	
COMMENT	

Department of Genetics Washington University Medical School Box 8322, 4566 Scott Ave., St. Louis, MO 63110, USA Tel: 314 362 2735 Fax: 314 362 7855 Email: mj@genetics.wustl.edu Class: random plasmid subclone. Location/Qualifiers									
FEATURES									
Source									
1. .56 /organism="Saccharomyces kluyveri" /strain="NRRL Y-12651 (CBS 3082)" /db_xref="taxon:4934" /clone="479.d1157f11.s1" /clone_lib="Saccharomyces kluyveri" /note="Random genomic sequence "									
BASE COUNT									
12 a 11 c 13 g 20 t									
ORIGIN									
Query Match 52.4%; Score 15.2; DB 13; Length 56; Best Local Similarity 71.4%; Pred. NO. 1.2e+05; Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;									
OY	1	tttgcttggtgcgtgcgttcgtttc 28							
Db	13	TTTGGTTTGTCGTGAGTGAATACCTTC 40							
RESULT 8									
AZ307056									
LOCUS									
1M0008G23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic									
DEFINITION									
clone UUGCIM0008G23 F, DNA sequence.									
ACCESSION									
AZ307056									
VERSION									
AZ307056.1 GI:10345677									
KEYWORDS									
GSS.									
SOURCE									
house mouse.									
Mus musculus									
ORGANISM									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.									
REFERENCE									
1 (bases 1 to 26)									
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.									
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts									
TITLE									
Unpublished (2000)									
JOURNAL									
Contact: Robert B. Weiss									
University of Utah Genome Center									
COMMENT									
University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0008 row: G column: 23 Seq primer: CGTGTAAACGACGCGCCACT Class: plasmid ends High quality sequence stop: 26. Location/Qualifiers									
1. .26 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGCIM0008G23" /clone_lib="Mouse 10kb plasmid UUGCIM library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource									
FEATURES									
Source									

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321149b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 0 a 2 c 11 g 13 t
ORIGIN

Query Match 51.7%; Score 15; DB 13; Length 26;
Best Local Similarity 78.3%; Pred. No. 1.5e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ttgcttggtgctgctgctgctg 23
|||||
Db 4 TCTGGCTTTGGTGGTGTCTG 26

RESULT 9
A2330732 36 bp DNA GSS 29-SEP-2000
LOCUS A2330732/c
DEFINITION 1M0056D12F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0056D12 F, DNA sequence.
ACCESSION A2330732
VERSION A2330732.1 GI:10392727
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 36)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: D column: 12
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 36.

TITLE
JOURNAL
COMMENT
FEATURES
SOURCE
1. 36
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0056D12"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321149b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 24 a 10 c 0 g 2 t
ORIGIN

Query Match 51.0%; Score 14.8; DB 13; Length 36;
Best Local Similarity 73.1%; Pred. No. 1.7e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 2 ttgcttggtgctgctgctgctg 27
|||||
Db 31 TTGGTTTGTGTTTGTGTTTGT 6

RESULT 10
A2330739 39 bp DNA GSS 29-SEP-2000
LOCUS A2330739/c
DEFINITION 1M0056F12F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0056F12 F, DNA sequence.
ACCESSION A2330739
VERSION A2330739.1 GI:10392741
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 39)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: F column: 12
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 39.

TITLE
JOURNAL
COMMENT
FEATURES
SOURCE
1. 39
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0056F12"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 25 a 12 c 0 g 2 t
ORIGIN

Query Match 51.0%; Score 14.8; DB 13; Length 39;
Best Local Similarity 73.1%; Pred. No. 1.7e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 2 ttggttgcgcgtcgtcgtt 27
Db 33 TTGCTTTTGTGTTTGTGTTT 8

RESULT 11
LOCUS A2424808 58 bp DNA GSS 03-OCT-2000
DEFINITION IM0204A07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION A2424808
VERSION A2424808.1 GI:10548821
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0204 row: A column: 07
Seq primer: CACACAGAAACAGCATGACC
Class: plasmid ends
High quality sequence stop: 58.
Location/Qualifiers
1. .58
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="UUGC1M0204A07"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"

FEATURES
source

1. .58
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="UUGC1M0204A07"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"

/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 1 c 17 g 33 t
ORIGIN

Query Match 51.0%; Score 14.8; DB 13; Length 58;
Best Local Similarity 73.1%; Pred. No. 1.6e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 ttggttgcgcgtcgtcgtt 26
Db 30 TTTTGTGTTTGTGTTTGTGTTT 55

RESULT 12
LOCUS AA405801 60 bp mRNA EST 09-NOV-1997
DEFINITION Z57F07.s1 Soares ovary tumor NBH07 Homo sapiens cDNA clone
ACCESSION AA405801
VERSION AA405801.1 GI:2063784
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
1 (bases 1 to 60)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, C., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Matra, M., Martin, J., Moore, B., Schellenberg, K., Stepovec, M., Tan, F., Theisling, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.
Insert Length: 171 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham.
Location/Qualifiers
1. .60
/organism="Homo sapiens"
/db_xref="GDB:5942423"
/db_xref="taxon:9606"
/clone="IMAGE:742117"
/clone_lib="Soares ovary tumor NBH07"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pTV73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

FEATURES
source

1. .60
/organism="Homo sapiens"
/db_xref="GDB:5942423"
/db_xref="taxon:9606"
/clone="IMAGE:742117"
/clone_lib="Soares ovary tumor NBH07"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pTV73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gdb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 21 g 37 t

ORIGIN

Query Match 50.3%; Score 14.6; DB 13; Length 58;
Best Local Similarity 81.0%; Pred. No. 1.9e+05;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 ttgtgctgctgctgctgttt 27
||||| ||||| ||||| ||||| |||||
Db 25 TTGTGTTGTTGTTGTTGTTT 45

RESULT 15
A2459776 41 bp DNA GSS 04-OCT-2000
LOCUS A2459776
DEFINITION 1M0264A19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION A2459776
VERSION A2459776.1 GI:10617901
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 41)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.,
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: A column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers

FEATURES

1. 41
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0264A19"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gdb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 3 c 12 g 24 t

ORIGIN

Query Match 49.7%; Score 14.4; DB 13; Length 41;
Best Local Similarity 75.0%; Pred. No. 2.3e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 ggccttgctgctgctgctgttt 27
|| ||| || ||||| ||| ||| ||
Db 4 GCTTTTGTGTCGATCTTGT 27

Search completed: March 9, 2002, 00:09:17
Job time: 11033 sec

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